

REMARKS

This Amendment, filed in reply to the Office Action dated April 14, 2008, is believed to be fully responsive to each point of objection and rejection raised therein. Accordingly, favorable reconsideration on the merits is respectfully requested.

Claims 13-15 are all the claims pending in the application. Claims 13-15 are rejected. Claims 13 and 14 are amended herewith. Support for these amendments can be found throughout the specification, at and, for example, Figure 1 and Example 1 of the specification as filed. Entry and consideration of this amendment are respectfully requested.

Claim to Priority

Applicants thank the Examiner for acknowledging Applicants' claim to foreign priority, and acknowledging receipt of all the priority documents.

Drawings

Applicants thank the Examiner for acknowledging acceptance of the Drawings filed September 11, 2007.

Claim 13 is Patentable Under 35 U.S.C. § 102

On page 2 of the Office Action, the Examiner maintains the rejection of Claim 13 under 35 U.S.C. 102(b) as being anticipated by Hayes *et al.* (*Journal of Clinical Pathology*, 1999, 52:97-103), as evidenced by Kondo *et al.* (U.S. Patent No. 5,853,981, issued December 29, 1998), for those reasons set forth in the Office Action mailed November 30, 2007.

In making the rejection, the Examiner asserts that Hayes *et al.* disclose step (A) of instant Claim 13 by obtaining RNA transcripts from human individuals infected with Epstein-Barr virus (EBV). In this regard, the Examiner asserts that the “selected DNA molecule” is the EBV genomic sequence. Regarding step (B), although the Examiner acknowledges that Hayes *et al.* do not disclose the technical details of the amplification reaction, the Examiner refers to Kondo *et al.* to assert that steps (B)(i)(a)-(B)(i)(e) of instant Claim 13 are an inherent property of the NASBA method performed by Hayes *et al.*

Regarding step (C) of instant Claim 13, the Examiner asserts that Hayes *et al.* disclose a method for screening at least 3 selected portions of the EBV DNA genome. The Examiner asserts that each portion (i.e., vIL-10, BDLF2, and BARF1) is different from, nonoverlapping with, and adjacent to the other portions, as evidenced by Table 3 of Hayes *et al.* In this regard, the Examiner asserts that the phrase “adjacent to,” absent a limiting description in the specification, may be defined as (a) not distant; (b) having a common endpoint or border; or (c) immediately preceding or following. In view of such definitions, the Examiner asserts that the vIL-10 gene, BDFL2 gene, and BARF1 gene are properly considered adjacent to one another, despite the presence of intervening sequences, because they are all located on the same genomic DNA molecule.

Applicants respectfully disagree. Applicants respectfully submit that Hayes *et al.*, as evidenced by Kondo *et al.*, do not teach each and every element of Claim 13, as is required to maintain a finding of anticipation. Specifically, neither Hayes *et al.* nor Kondo *et al.* disclose step (B)(i)(c) of Claim 13, namely wherein “said second primer further comprises an RNA-transcriptable promoter sequence at its 5'-end ...” Applicants point out that in the instant method, the primer containing the RNA-transcriptable promoter is used in conjunction with a

DNA-dependent DNA polymerase to synthesize a double-stranded DNA molecule. Thus, the claimed method is distinct to that of Kondo *et al.*, since Kondo *et al.* do not utilize an RNA-transcriptable promoter sequence on the primer that mediates double-stranded DNA product formation. Rather, in the method disclosed by Kondo *et al.*, only the primer mediating RNA/DNA hybrid formation (i.e., said first primer) contains an RNA-transcriptable promoter sequence. See Column 4, lines 30-38. Accordingly, Hayes *et al.*, as evidenced by Kondo *et al.*, fail to teach each and every element of Claim 13, as is required to maintain a finding of anticipation. Thus, Claim 13 is not anticipated for at least this reason.

Nevertheless, in the interest of compact prosecution, and without acquiescing in the rejection, Applicants herewith amend Claim 13 to even further clarify Applicants' claimed invention. Specifically, step (C) of Claims 13 and 14 is amended herewith to recite that the selected portions are "not separated by any intervening nucleotides on said selected DNA molecule." Support for such an amendment can be found in Figure 1 and is inherent in Example 1 of the specification as filed. Thus, Claim 13 is not anticipated by Hayes *et al.* or Kondo *et al.* at least because the vIL-10, BDFL2, and BARF1 genes of Hayes *et al.* are separated by thousands of intervening nucleotides on the selected DNA molecule. Thus, for this reason also, Hayes *et al.*, as evidenced by Kondo *et al.*, fail to teach each and every element of Claim 13 as amended, as is required to maintain a finding of anticipation.

Thus, in view of the foregoing, Applicants respectfully submit that Claim 13 is not anticipated by Hayes *et al.*, as evidenced by Kondo *et al.*

Withdrawal of the rejection is respectfully requested.

Claims 14 and 15 are Patentable Under 35 U.S.C. § 103

On page 5 of the Office Action, the Examiner maintains the rejection of Claims 14 and 15 under 35 U.S.C. 103(a) as being unpatentable over Hayes *et al.* (*Journal of Clinical Pathology*, 1999, 52:97-103), as evidenced by Kondo *et al.* (U.S. Patent No. 5,853,981, issued December 29, 1998) as applied to Claim 13 above, and further in view of Ishiguro *et al.* (*Nucleic Acids Research*, 1996, vol. 24, No. 24), for those same reasons as set forth in the Office Action mailed November 30, 2007.

In making the rejection, the Examiner acknowledges that Hayes *et al.*, as evidenced by Kondo *et al.*, do not disclose a probe labeled with an intercalating fluorescent dye. In an attempt to rectify this deficiency, the Examiner cites to Ishiguro *et al.*, who allegedly disclose a fluorescent intercalative dye-labeled probe which can recognize a specific nucleic acid sequence by linking of a fluorescent intercalative dye as a label to a single-stranded oligonucleotide that is complementary in sequence to a specific nucleic acid sequence. The Examiner asserts that one of ordinary skill in the art would have been motivated to use the probes described by Ishiguro *et al.* with the method of Hayes *et al.* since they enable detection and quantification of nucleotide specific hybrids, not just any double stranded hybrid.

Applicants respectfully disagree.

As mentioned above, Hayes *et al.*, as evidenced by Kondo *et al.*, fail to teach each and every element of Claim 13. The addition of Ishiguro *et al.* does not compensate for the deficiencies of the primary references since Ishiguro *et al.* only disclose the use of a fluorescently-labeled oligonucleotide. Thus, Hayes *et al.*, Kondo *et al.* and Ishiguro *et al.*, taken alone or in combination, fail to teach each and every element of the claims, as is required to

maintain a rejection under 35 U.S.C. § 103. Accordingly, the cited references do not render obvious Claims 14 and 15.

Withdrawal of the rejection is respectfully requested.

Conclusion

In view of the above, reconsideration and allowance of this application are now believed to be in order, and such actions are hereby solicited. If any points remain in issue which the Examiner feels may be best resolved through a personal or telephone interview, the Examiner is kindly requested to contact the undersigned at the telephone number listed below.

The USPTO is directed and authorized to charge all required fees, except for the Issue Fee and the Publication Fee, to Deposit Account No. 19-4880. Please also credit any overpayments to said Deposit Account.

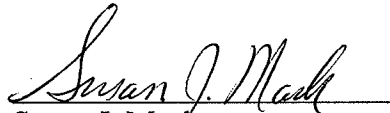
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